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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/301,766DATE: 05/10/1999
TIME: 14:12:10

Input Set: I301766.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

W--> 1 <110> APPLICANT: Eijiro WATANABE
2 Kenji OEDA
3 <120> TITLE OF INVENTION: Raffinose Synthase Genes and Their Use
4 <130> FILE REFERENCE:
5 <140> CURRENT APPLICATION NUMBER: US/09/301,766
6 <141> CURRENT FILING DATE: 1999-04-29
7 <150> EARLIER APPLICATION NUMBER: JP 10/120550
8 <151> EARLIER FILING DATE: 1998-04-30
9 <150> EARLIER APPLICATION NUMBER: JP 10/120551
10 <151> EARLIER FILING DATE: 1998-04-30
11 <150> EARLIER APPLICATION NUMBER: JP 10/345590
12 <151> EARLIER FILING DATE: 1998-12-04
13 <150> EARLIER APPLICATION NUMBER: JP 10/351246
14 <151> EARLIER FILING DATE: 1998-12-10
15 <160> NUMBER OF SEQ ID NOS: 53
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17 <211> LENGTH: 265
18 <212> TYPE: PRT
19 <213> ORGANISM: Glycine max
20 <400> SEQUENCE: 1
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22 5 10 15
23 Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Lys His Asn Phe
24 20 25 30
25 Lys Leu Leu Lys Lys Leu Val Leu Pro Asp Gly Ser Ile Leu Arg Cys
26 35 40 45
27 Gln His Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe Val Asp Pro Leu
28 50 55 60
29 His Asp Gly Lys Thr Met Leu Lys Ile Trp Asn Leu Asn Lys Cys Ser
30 65 70 75 80
31 Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly Trp Cys Pro Val
32 85 90 95
33 Thr Arg Arg Asn Lys Ser Ser Ser Asp Tyr Ser His Ser Val Thr Cys
34 100 105 110
35 Phe Ala Ser Pro Gln Asp Ile Glu Trp Gly Lys Gly Lys His Pro Val
36 115 120 125
37 Cys Ile Lys Gly Val Asp Val Phe Ala Val Tyr Met Phe Lys Asp Asp
38 130 135 140
39 Lys Leu Lys Leu Leu Lys Tyr Thr Glu Ser Val Glu Val Ser Leu Glu
40 145 150 155 160
41 Pro Phe Ser Cys Glu Leu Leu Thr Val Ser Pro Val Val Ile Leu Pro
42 165 170 175
43 Arg Lys Ser Ile Gln Phe Ala Pro Ile Gly Leu Val Asn Met Leu Asn
44 180 185 190

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45      Ser Gly Gly Ser Ile Met Ser Leu Glu Phe Asp Gln Gln Glu Asn Leu
46              195                      200                      205
47      Ala Arg Ile Gly Val Arg Gly His Gly Glu Met Arg Val Phe Ala Ser
48              210                      215                      220
49      Glu Lys Pro Glu Ser Val Lys Ile Asp Gly Glu Ser Val Glu Phe Asp
50      225                      230                      235                      240
51      Tyr Val Asp Arg Thr Val Arg Leu Gln Val Ser Trp Pro Cys Ser Ser
52              245                      250                      255
53      Arg Leu Ser Val Val Glu Tyr Leu Phe
54              260                      265
55      <210> SEQ ID NO 2
56      <211> LENGTH: 928
57      <212> TYPE: DNA
58      <213> ORGANISM: Glycine max
59      <220> FEATURE:
60      <221> NAME/KEY: CDS
61      <222> LOCATION: (2)...(799)
62      <400> SEQUENCE: 2
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66      att tct ggt gga cca att tat gta agc gac tct gtt gga aaa cac aac      94
67      Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Lys His Asn
68              20                      25                      30
69      ttc aag ttg ctt aag aag ctt gtt cta cct gat ggc tcc att ttg cgg      142
70      Phe Lys Leu Leu Lys Lys Leu Val Leu Pro Asp Gly Ser Ile Leu Arg
71              35                      40                      45
72      tgt caa cat tat gca ctt ccc acc cga gac tgc tta ttt gta gat cct      190
73      Cys Gln His Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe Val Asp Pro
74              50                      55                      60
75      tta cat gat ggg aaa aca atg ctc aaa att tgg aac ctc aat aaa tgt      238
76      Leu His Asp Gly Lys Thr Met Leu Lys Ile Trp Asn Leu Asn Lys Cys
77              65                      70                      75
78      tcc ggg gtt ttg ggt ctg ttc aat tgc caa gga gga ggt tgg tgc cct      286
79      Ser Gly Val Leu Gly Leu Phe Asn Cys Gln Gly Gly Gly Trp Cys Pro
80      80                      85                      90                      95
81      gtt act agg cga aac aag agt agc tct gac tat tca cac tcc gtg act      334
82      Val Thr Arg Arg Asn Lys Ser Ser Ser Asp Tyr Ser His Ser Val Thr
83              100                      105                      110
84      tgc ttt gca agt cct caa gac att gaa tgg ggc aaa ggg aag cac cca      382
85      Cys Phe Ala Ser Pro Gln Asp Ile Glu Trp Gly Lys Gly Lys His Pro
86              115                      120                      125
87      gtt tgc atc aaa ggg gtg gac gta ttt gct gtg tac atg ttt aag gac      430
88      Val Cys Ile Lys Gly Val Asp Val Phe Ala Val Tyr Met Phe Lys Asp
89              130                      135                      140
90      gac aag ttg aag ctg ctg aag tac aca gag agt gta gaa gtt tct ctt      478
91      Asp Lys Leu Lys Leu Leu Lys Tyr Thr Glu Ser Val Glu Val Ser Leu
92              145                      150                      155
93      gag cct ttt agt tgt gag ctt ttg acc gtt tct cca gtg gtg atc tta      526
94      Glu Pro Phe Ser Cys Glu Leu Leu Thr Val Ser Pro Val Val Ile Leu

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95      160      165      170      175
96      ccc aga aaa tca atc caa ttt gcc cca att gga ttg gta aac atg ctc      574
97      Pro Arg Lys Ser Ile Gln Phe Ala Pro Ile Gly Leu Val Asn Met Leu
98      180      185      190
99      aac tct ggg ggc tct att atg tca ttg gaa ttt gat caa cag gaa aat      622
100     Asn Ser Gly Gly Ser Ile Met Ser Leu Glu Phe Asp Gln Gln Glu Asn
101     195      200      205
102     ttg gcg agg att ggg gtg aga gga cat ggg gaa atg agg gta ttt gca      670
103     Leu Ala Arg Ile Gly Val Arg Gly His Gly Glu Met Arg Val Phe Ala
104     210      215      220
105     tca gag aag cca gag agt gtc aag att gat gga gaa tct gtg gaa ttt      718
106     Ser Glu Lys Pro Glu Ser Val Lys Ile Asp Gly Glu Ser Val Glu Phe
107     225      230      235
108     gat tat gtt gat aga acc gtg agg ctc caa gtc tcg tgg cct tgt tct      766
109     Asp Tyr Val Asp Arg Thr Val Arg Leu Gln Val Ser Trp Pro Cys Ser
110     240      245      250      255
111     tcg agg ttg tcc gta gtc gag tat ttg ttc tga atcatgattt ggtgtccgag      819
112     Ser Arg Leu Ser Val Val Glu Tyr Leu Phe
113     260      265
114     agagccgtgt aatgttcaca taaactgact taagtgcatt aagcaaatcc accttaaata      879
115     atagtgcata actttgttcc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      928
116     <210> SEQ ID NO 3
117     <211> LENGTH: 783
118     <212> TYPE: PRT
119     <213> ORGANISM: Beta vulgaris L.
120     <400> SEQUENCE: 3
121     Met Ala Pro Ser Phe Ser Lys Glu Asn Ser Lys Thr Cys Asp Glu Val
122     5      10      15
123     Ala Asn His Asp Asp Cys Asn Thr Cys Pro Ile Ile Ser Leu Glu Glu
124     20      25      30
125     Ser Asn Phe Met Val Asn Gly His Val Ile Leu Ser Gln Val Pro Ser
126     35      40      45
127     Asn Ile Thr Ala Ile Ser Lys Met Gly Phe Asp Gly Leu Phe Val Gly
128     50      55      60
129     Phe Asp Ala Pro Glu Pro Lys Ala Arg His Val Val Ser Val Gly Gln
130     65      70      75      80
131     Leu Lys Gly Ile Pro Phe Met Ser Ile Phe Arg Phe Lys Val Trp Trp
132     85      90      95
133     Thr Thr His Trp Thr Gly Ser Asn Gly Arg Asp Leu Glu His Glu Thr
134     100     105     110
135     Gln Ile Leu Ile Leu Asp Lys Ser Asp Glu Gly Leu Gly Arg Pro Tyr
136     115     120     125
137     Ile Val Ile Leu Pro Leu Ile Glu Gly Pro Phe Arg Ala Ser Leu Gln
138     130     135     140
139     Pro Gly Ser Val Asp Asp Tyr Val Asp Ile Cys Val Glu Ser Gly Ser
140     145     150     155     160
141     Thr Lys Val Val Gly Asp Ser Phe Arg Ala Val Leu Tyr Ile Arg Ala
142     165     170     175
143     Gly Pro Asp Pro Phe Lys Leu Ile Lys Asp Thr Met Lys Glu Val Gln
144     180     185     190

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145	Ala	His	Leu	Gly	Thr	Phe	Lys	Leu	Leu	Asp	Asp	Lys	Thr	Pro	Pro	Gly
146			195					200					205			
147	Ile	Val	Asp	Lys	Phe	Gly	Trp	Cys	Thr	Trp	Asp	Ala	Phe	Tyr	Leu	Lys
148			210				215					220				
149	Val	Glu	Pro	Tyr	Gly	Val	Trp	Glu	Gly	Val	Lys	Gly	Leu	Val	Glu	Asn
150			225				230					235				240
151	Gly	Val	Pro	Pro	Gly	Leu	Val	Leu	Ile	Asp	Asp	Gly	Trp	Gln	Ser	Ile
152					245					250					255	
153	Cys	His	Asp	Asp	Asp	Pro	Ile	Thr	Asp	Gln	Glu	Gly	Ile	Asn	Arg	Thr
154				260					265					270		
155	Ser	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	Leu	Ile	Lys	Tyr	Glu	Glu	Asn
156			275					280					285			
157	Phe	Lys	Phe	Arg	Asp	Tyr	Lys	Ser	Pro	Asn	Ile	Met	Gly	His	Glu	Asp
158			290				295					300				
159	His	Pro	Asn	Met	Gly	Met	Arg	Ala	Phe	Val	Arg	Asp	Leu	Lys	Glu	Glu
160			305			310					315					320
161	Phe	Lys	Thr	Val	Glu	His	Val	Tyr	Val	Trp	His	Ala	Phe	Thr	Gly	Tyr
162				325						330					335	
163	Trp	Gly	Gly	Val	Arg	Pro	Asn	Val	Pro	Gly	Leu	Pro	Glu	Ala	Gln	Val
164				340					345					350		
165	Val	Thr	Pro	Lys	Leu	Ser	Pro	Gly	Leu	Glu	Met	Thr	Met	Glu	Asp	Leu
166			355					360					365			
167	Ala	Val	Asp	Lys	Ile	Val	Asn	Asn	Gly	Ile	Gly	Leu	Val	Gln	Pro	Asp
168			370				375					380				
169	Lys	Ala	Gln	Glu	Leu	Tyr	Glu	Gly	Leu	His	Ser	His	Leu	Glu	Asn	Cys
170			385			390					395					400
171	Gly	Ile	Asp	Gly	Val	Lys	Val	Asp	Val	Ile	His	Leu	Leu	Glu	Met	Met
172				405						410					415	
173	Ala	Glu	Asp	Tyr	Gly	Gly	Arg	Val	Glu	Leu	Ala	Lys	Thr	Tyr	Tyr	Lys
174				420					425					430		
175	Ala	Ile	Thr	Glu	Ser	Val	Arg	Lys	His	Phe	Lys	Gly	Asn	Gly	Val	Ile
176			435					440					445			
177	Ala	Ser	Met	Glu	Gln	Cys	Asn	Asp	Phe	Met	Leu	Leu	Gly	Thr	Glu	Thr
178			450				455						460			
179	Ile	Cys	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Pro	Thr	Asp	Pro	Ser
180			465			470					475					480
181	Gly	Asp	Ile	Asn	Gly	Thr	Tyr	Trp	Leu	Gln	Gly	Cys	His	Met	Val	His
182				485						490					495	
183	Cys	Ala	Tyr	Asn	Ser	Leu	Trp	Met	Gly	Asn	Phe	Ile	His	Pro	Asp	Trp
184				500					505					510		
185	Asp	Met	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Glu	Phe	His	Ala	Ala	Ser
186			515					520					525			
187	Arg	Ala	Ile	Ser	Gly	Gly	Pro	Ile	Tyr	Val	Ser	Asp	Val	Val	Gly	Lys
188			530				535						540			
189	His	Asn	Ile	Pro	Leu	Leu	Lys	Arg	Leu	Val	Leu	Ala	Asp	Gly	Ser	Ile
190			545			550					555					560
191	Leu	Arg	Cys	Glu	Tyr	His	Ala	Leu	Pro	Thr	Lys	Asp	Cys	Leu	Phe	Val
192				565						570					575	
193	Asp	Pro	Leu	His	Asp	Gly	Lys	Thr	Met	Leu	Lys	Ile	Trp	Asn	Leu	Asn
194				580					585					590		

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195      Lys Tyr Asn Gly Val Leu Gly Val Phe Asn Cys Gln Gly Gly Gly Trp
196              595                      600                      605
197      Ser Arg Glu Ser Arg Lys Asn Leu Cys Phe Ser Glu Tyr Ser Lys Pro
198              610                      615                      620
199      Ile Ser Cys Lys Thr Ser Pro Lys Asp Val Glu Trp Glu Asn Gly His
200      625                      630                      635                      640
201      Lys Pro Phe Pro Ile Lys Gly Val Glu Cys Phe Ala Met Tyr Phe Thr
202              645                      650                      655
203      Lys Glu Lys Lys Leu Ile Leu Ser Gln Leu Ser Asp Thr Ile Glu Ile
204              660                      665                      670
205      Ser Leu Asp Pro Phe Asp Tyr Glu Leu Ile Val Val Ser Pro Met Thr
206              675                      680                      685
207      Ile Leu Pro Trp Glu Ser Ile Ala Phe Ala Pro Ile Gly Leu Val Asn
208              690                      695                      700
209      Met Leu Asn Ala Gly Gly Ala Val Lys Ser Leu Asp Ile Ser Glu Asp
210      705                      710                      715                      720
211      Asn Glu Asp Lys Met Val Gln Val Gly Ile Lys Gly Ala Gly Glu Met
212              725                      730                      735
213      Met Val Tyr Ser Ser Glu Lys Pro Lys Ala Cys Arg Val Asn Gly Glu
214              740                      745                      750
215      Asp Met Glu Phe Glu Tyr Glu Glu Ser Met Ile Lys Val Gln Val Thr
216              755                      760                      765
217      Trp Asn His Asn Ser Gly Gly Phe Thr Thr Val Glu Tyr Leu Phe
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219 <210> SEQ ID NO 4
220 <211> LENGTH: 2690
221 <212> TYPE: DNA
222 <213> ORGANISM: Beta vulgaris L.
223 <220> FEATURE:
224 <221> NAME/KEY: CDS
225 <222> LOCATION: (236)...(2587)
226 <400> SEQUENCE: 4

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228      ttcattgtta agattttgta attgaattca aattcttaat tctgaatttt gtcatttttt      120
229      ttgtggggat atttataact atcatattat ttgtgtagat cattctacaa aaaagagagt      180
230      gagttttttt agctcttatt tcctaagaaa ttaatagcaa aagttttgca taact atg      238
231                                         Met
232
233      gct cca agc ttt agc aag gaa aat tcc aag acg tgt gat gag gtt gca      286
234      Ala Pro Ser Phe Ser Lys Glu Asn Ser Lys Thr Cys Asp Glu Val Ala
235              5                      10                      15
236      aac cat gat gat tgc aac acg tgt cca ata att tcc ttg gaa gaa tca      334
237      Asn His Asp Asp Cys Asn Thr Cys Pro Ile Ile Ser Leu Glu Glu Ser
238              20                      25                      30
239      aac ttc atg gtg aat ggt cac gtg ata ttg tcc caa gtt cca tcc aac      382
240      Asn Phe Met Val Asn Gly His Val Ile Leu Ser Gln Val Pro Ser Asn
241              35                      40                      45
242      atc acg gcc att agt aaa atg ggt ttt gat ggg ctt ttt gtg ggt ttt      430
243      Ile Thr Ala Ile Ser Lys Met Gly Phe Asp Gly Leu Phe Val Gly Phe
244              50                      55                      60                      65

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I301766.RAW

Line	? Error/Warning	Original Text
4	W Response to "File Reference" is Missing	
232	W Invalid/Missing Amino Acid Numbering	
956	W "N" or "Xaa" used: Feature required	cgatggatgg gnaanttntat ncancngan tggganat
965	W "N" or "Xaa" used: Feature required	ggccacatnt tnacnarncc natngngcn aa
983	W "N" or "Xaa" used: Feature required	cgaggnggnt gnccncngg nttngtatn atnganga
992	W "N" or "Xaa" used: Feature required	atyttrtcna cngcnarrtc ytccatngt
1001	W "N" or "Xaa" used: Feature required	ggnacntant ggytncangg ntgnacanatg gtncantg
1010	W "N" or "Xaa" used: Feature required	ggccacatnt tnacnarncc natngngcn aa
1091	W "N" or "Xaa" used: Feature required	cgattnaang tntgggtggac nacncantgg gtngg
1100	W "N" or "Xaa" used: Feature required	cantgnacca tntgncancc ntgnarccan tangtncc